

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/009,030
Source: P45/10
Date Processed by STIC: 11/6/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 10/009,030

TN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

Skipped Sequences
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

Use of <220>
 - - - - - Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

Misuse of n
 - - - - - n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



PCT/0

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/009,030

DATE: 11/06/2002
TIME: 14:11:23

Input Set : A:\410.txt
Output Set: N:\CRF4\11062002\J009030.raw

9 <110> APPLICANT: Arand, Michel
10 Archelas, Alain Robert
11 Baratti, Jacques
12 Furstoss, Roland
14 <120> TITLE OF INVENTION: PROTEINS WITH FUNGICIDAL ORIGIN AND DERIVATIVES, THEIR
15 PROCESS OF OBTENTION, AND THEIR USES, NAMELY FOR THE
16 PREPARATION OF ENANTIOMERICALLY PURE MOLECULES
18 <130> FILE REFERENCE: 410.018
20 <140> CURRENT APPLICATION NUMBER: 10/009,030
21 <141> CURRENT FILING DATE: 2000-11-02
23 <160> NUMBER OF SEQ ID NOS: 2
25 <170> SOFTWARE: PatentIn Ver. 2.1

ERRONEOUS SEQUENCES

27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1197
29 <212> TYPE: DNA
30 <213> ORGANISM: Aspergillus niger
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(1197)
36 Nucleotide Sequence SEQ ID NO : 1 *it is
delete this - not necessary*

37 <400> SEQUENCE: 1
38 atg tcc gct ccg ttc gcc aag ttt ccc tcg tcg gcg agc att tcg cct 48
39 Met Ser Ala Pro Phe Ala Lys Phe Pro Ser Ser Ala Ser Ile Ser Pro
40 1 5 10 15
42 aat cct ttc acg gtc tct atc ccg gat gaa gag ttg gat gac ttg aaa 96
43 Asn Pro Phe Thr Val Ser Ile Pro Asp Glu (Gin) Leu Asp Asp Leu Lys
44 20 25 invalid 30 35 *misaligned number
(see item 3
in Error
Summary
Sheet)*
46 acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144
47 Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
48 35 40 45
50 caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg 192
51 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
52 50 55 60
54 cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga 240
55 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
56 65 70 75 80
58 ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att 288
59 Leu Asn Ser Phe Pro Gln Phe Thr Glu Ile Glu Gly Leu Thr Ile
60 85 90 95

RAW SEQUENCE LISTING
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Input Set : A:\410.txt
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62 cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca 336
 63 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
 --> 64 : 100 105 110
 66 ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg 384
 67 Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
 --> 68 115 120 125
 70 cag cta ttc cgg gag gag tac acc cct gag act ctg cca ttc cat ctg 432
 71 Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
 --> 72 130 135 140
 --> 74 gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg 480
 75 Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu
 --> 76 145 150 155 160
 78 gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg 528
 79 Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu
 --> 80 165 170 175
 82 atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat 576
 83 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp
 --> 84 180 185 190
 86 att ggt agc ttt gtt gga cga ctg ttg ggc gtc ggt ttc gac gcc tgc 624
 87 Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
 --> 88 195 200 205
 90 aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc 672
 91 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
 --> 92 210 215 220
 94 ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga 720
 95 Pro Ser Ile Glu Ser Leu Ala Ala Glu Lys Glu Gly Ile Ala Arg
 --> 96 225 230 235 240
 98 atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt 768
 99 Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser
 --> 100 245 align this number 250 255
 102 act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca 816 Under
 103 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Pro Ile Ala
 --> 104 260 265 270
 106 tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc 864
 107 Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro
 --> 108 275 280 285
 110 ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg 912
 111 Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr
 --> 112 290 295 300
 117 gaa agt ttc ccg cgg gca att cat acc tac cgc gag act acc cca act 960
 118 Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr
 --> 119 305 310 315 320
 121 gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att 1008
 122 Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
 --> 123 325 330 335
 125 cac aag ccg ttt ggg ttc tcc ttc ccc aag gac ctt tgt cct gtg 1056
 126 His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val
 --> 127 340 345 350
 129 cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat 1104

OK

align nos. directly
Under
Aminoacid

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Input Set : A:\410.txt
Output Set: N:\CRF4\11062002\J009030.raw

130 Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp
--> 131 355 360 365
133 cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg 1152
134 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu
7-> 135 370 375 380
137 aag acc gac ctg aca gca ttt gtc gag cag gtg tgg eaa aag tag 1197
--> 138 Lys Thr Asp Leu Thr Ala Phe Val Glu Gin Val Trp Gin Lys
--> 139 385 390 395
--> 141 Peptide sequence seq id no : 2
142 <210> SEQ ID NO: 2
143 <211> LENGTH: 399 delete invalid
--> 144 <212> TYPE: (mandatory response (insert PRT)) 398 shown below
145 <213> ORGANISM: Aspergillus niger
147 <400> SEQUENCE: 2
148 Met Ser Ala Pro Phe Ala Lys Phe Pro Ser Ser Ala Ser Ile Ser Pro
149 1 5 10 15
151 Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gin Leu Asp Asp Leu Lys
152 20 25 30
154 Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
155 35 40 45
157 Gin Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
158 50 55 60
160 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
161 65 75 80
163 Leu Asn Ser Phe Pro Gin Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
164 85 90 95
166 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
167 100 105 110
169 Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
170 115 120 125
173 Gin Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
174 130 135 140
176 Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu
177 145 150 155
179 Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gin Leu
180 165 170 175
182 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gin Gly Gly Asp
183 180 185 190
185 Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
186 195 200 205
188 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
189 210 215 220
191 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg
192 225 230 235 240
194 Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser
195 245 250 255
197 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala
198 260 265 270
200 Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro

→ invalid
amino acid
designation
(multiple
appearances
in the sequence)

move line over
so that
numbers
appear
directly
under
amino
acids

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DATE: 11/06/2002
TIME: 14:11:23

Input Set : A:\410.txt
Output Set: N:\CRF4\11062002\J009030.raw

201	275	280	285	
203	Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr			
204	290	295	300	
206	Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr			
207	305	310	315	320
209	Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu	Tyr Ile	delete one	
210	325	330	335	space
212	His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val			
213	340	345	350	
215	Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp			only one
216	355	360	365	space
218	His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu			
219	370	375	380	
221	Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys			between
222	385	390	395	amino acids

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/009,030

DATE: 11/06/2002

TIME: 14:11:24

Input Set : A:\410.txt

Output Set: N:\CRF4\11062002\J009030.raw

:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
:37 M:283 W: Missing Blank Line separator, <400> field identifier
:43 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:52 M:336 W: Invalid Amiro Acid Number in Coding Region, SEQ ID:1
:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:74 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:100 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:138 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:141 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:1
:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1196
:141 M:254 E: No. of Bases conflict, LENGTH:Input:2 Counted:1220 SEQ:1
:141 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
:141 M:112 C: (48) String data converted to lower case,
:141 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1197 Found:1220 SEQ:1
:144 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: